

DAVI251.001APC_sequence listing.TXT
SEQUENCE LISTING

<110> Melbourne Health
Jane, Stephen (US Only)
Wilanowski, Tomasz (US only)
Ting, Stephen (US only)

<120> MAMMALIAN GRAINYHEAD TRANSCRIPTION FACTORS

<130> DAVI251.001APC

<140> US 10/524,619
<141> 2005-02-09

<150> PCT/AU03/01006
<151> 2003-08-08

<150> US 60/402055
<151> 2002-08-09

<150> AU2002951579
<151> 2002-08-22

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<170> PatentIn version 3.1

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Met Ala Ser Leu Trp Glu Ser
1 5

ccc cag cag tgt atc atc ctg agc cca ctg agc ggg tgg tgg ttt tcg 162
Pro Gln Gln Cys Ile Ile Ser Pro Leu Ser Gly Trp Trp Phe Ser
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atc gga atc tca ata ctg acc agt tca gct ctg gtg ctc aag ccc caa 210
Ile Gly Ile Ser Ile Leu Thr Ser Ser Ala Leu Val Leu Lys Pro Gln
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atg ctc aaa ggc gaa ctc cag act cga cct tct cag aga cct tca agg 258
Met Leu Lys Gly Glu Leu Gln Thr Arg Pro Ser Gln Arg Pro Ser Arg
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aag gcg ttc agg agg aac aac ttt gaa tat acc cta gaa gct tca aaa 306
Lys Ala Phe Arg Arg Asn Asn Phe Glu Tyr Thr Leu Glu Ala Ser Lys
60 65 70

tca ctt cga cag aag cca gga gac agt acc atg acg tac ctg aac aaa 354
Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr Met Thr Tyr Leu Asn Lys
75 80 85

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ggc cag ttc tat ccc atc acc ttg aag gag gtg agc agc agt gaa gga	402
Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu Val Ser Ser Ser Glu Gly	
90 95 100	
atc cat cat ccc atc agc aaa gtt cga agt gtg atc atg gtg gtt ttt	450
Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile Met Val Val Phe	
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gct gaa gac aaa agc aga gaa gat cag tta agg cat tgg aag tac tgg	498
Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His Trp Lys Tyr Trp	
120 125 130 135	
cac tcc cgg cag cac acc gct aaa caa aga tgc att gac ata gct gac	546
His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile Asp Ile Ala Asp	
140 145 150	
tat aaa gaa agc ttc aac act atc agt aac atc gag gag att gcg tat	594
Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu Glu Ile Ala Tyr	
155 160 165	
aac gcc att tcc ttc aca tgg gac atc aac gat gaa gca aag gtt ttc	642
Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu Ala Lys Val Phe	
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atc tct gtg aac tgc tta agc aca gat ttc tct tcc cag aag gga gtg	690
Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val	
185 190 195	
aag ggg ttg cct ctt aac att caa gtt gat acc tat agt tac aac aac	738
Lys Gly Leu Pro Leu Asn Ile Gln Val Asp Thr Tyr Ser Tyr Asn Asn	
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cgc agc aac aag cct gtg cac cgg gcc tac tgc cag atc aag gtc ttc	786
Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln Ile Lys Val Phe	
220 225 230	
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Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln	
235 240 245	
agc aaa aga aaa gtt tct gat gtt aaa gtg cca ctg ctt ccc tct cac	882
Ser Lys Arg Lys Val Ser Asp Val Lys Val Pro Leu Leu Pro Ser His	
250 255 260	
aag cga atg gat atc aca gtt ttc aaa ccc ttc att gat ctc gat act	930
Lys Arg Met Asp Ile Thr Val Phe Lys Pro Phe Ile Asp Leu Asp Thr	
265 270 275	
cag cct gtc ctc ttc att cct gac gtg cac ttt gcc aac ttg cag cgg	978
Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg	
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Gly Thr His Val Leu Pro Ile Ala Ser Glu Glu Leu Glu Gly Glu Gly	
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tct gtc ttg aaa agg ggg ccg tac ggc aca gaa gat gac ttt gct gtc	1074
Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr Glu Asp Asp Phe Ala Val	
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330

335

340

ctc tac gtt cga aag gag tca gaa gaa gtc ttt gat gcc ctg atg ctc	1170
Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp Ala Leu Met Leu	
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aaa acc cca tct ttg aag ggc ttg atg gaa gct atc tca gac aaa tac	1218
Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile Ser Asp Lys Tyr	
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gat gtt ccc cat gac aag att ggg aaa ata ttc aag aag tgt aaa aag	1266
Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys Lys Cys Lys Lys	
380 385 390	
ggg atc ctg gtg aac atg gac gac aac att gtg aag cat tac tcc aat	1314
Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys His Tyr Ser Asn	
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Glu Asp Thr	
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Leu Ser Gly Trp Trp Phe Ser Ile Gly Ile Ser Ile Leu Thr Ser Ser	
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Ala Leu Val Leu Lys Pro Gln Met Leu Lys Gly Glu Leu Gln Thr Arg	
35 40 45	

Pro Ser Gln Arg Pro Ser Arg Lys Ala Phe Arg Arg Asn Asn Phe Glu	
50 55 60	

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Tyr Thr Leu Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser
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Thr Met Thr Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys
85 90 95

Glu Val Ser Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg
100 105 110

Ser Val Ile Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln
115 120 125

Leu Arg His Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln
130 135 140

Arg Cys Ile Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser
145 150 155 160

Asn Ile Glu Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile
165 170 175

Asn Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp
180 185 190

Phe Ser Ser Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val
195 200 205

Asp Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala
210 215 220

Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile
225 230 235 240

Arg Asp Glu Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys
245 250 255

Val Pro Leu Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys
260 265 270

Pro Phe Ile Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val
275 280 285

His Phe Ala Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser
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Glu Glu Leu Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly
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Thr Glu Asp Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile
 325 330 335

Glu Glu Pro Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu
 340 345 350

Val Phe Asp Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met
 355 360 365

Glu Ala Ile Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys
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 Gln Asn Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp
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gag gcc tgg aaa tcc ttc ctg gaa aac cct ctc act gca gcg acc aaa 144
 Glu Ala Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys
 35 40 45

gcg atg atg agc atc aat gga gat gaa gac agc gcc gct gcg ctg ggc 192
 Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly
 50 55 60

ctg ctc tat gac tac tac aag gtt cca aga gag aga agg tca tca aca 240
 Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Thr
 65 70 75

gca aag cca gag gtg gag cac cct gag cca gat cac agc aaa aga aac 288

DAVI251.001APC_sequence_listing.TXT

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Ser	Ile	Pro	Ile	Val	Thr	Glu	Gln	Pro	Leu	Ile	Ser	Ala	Gly	Glu	Asn	
95					100					105					110	
aga	gtg	caa	gta	ctg	aaa	aat	gtg	cca	ttt	aac	att	gtc	ctt	ccc	cat	384
Arg	Val	Gln	Val	Leu	Lys	Asn	Val	Pro	Phe	Asn	Ile	Val	Leu	Pro	His	
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ggc	aac	cag	ctg	ggc	att	gat	aag	aga	ggc	cat	ctg	aca	gct	tca	gat	432
Gly	Asn	Gln	Leu	Gly	Ile	Asp	Lys	Arg	Gly	His	Leu	Thr	Ala	Ser	Asp	
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acg	aca	gtc	act	gtc	tcc	ata	gca	acg	atg	cct	acc	cac	tcc	atc	aag	480
Thr	Thr	Val	Thr	Val	Ser	Ile	Ala	Thr	Met	Pro	Thr	His	Ser	Ile	Lys	
					145				150				155			
aca	gaa	acc	cag	cca	cat	ggc	ttc	gct	gtg	gga	atc	ccc	cca	gca	gtg	528
Thr	Glu	Thr	Gln	Pro	His	Gly	Phe	Ala	Val	Gly	Ile	Pro	Pro	Ala	Val	
					160				165				170			
tat	cat	cct	gag	ccc	act	gag	cgg	gtg	gtg	gtt	ttc	gat	cgg	aay	ctc	576
Tyr	His	Pro	Glu	Pro	Thr	Glu	Arg	Val	Val	Val	Phe	Asp	Arg	Asn	Leu	
					175				180			185			190	
aat	act	gac	cag	ttc	agc	tct	ggt	gct	caa	gcc	cca	aat	gct	caa	agg	624
Asn	Thr	Asp	Gln	Phe	Ser	Ser	Gly	Ala	Gln	Ala	Pro	Asn	Ala	Gln	Arg	
					195				200						205	
cga	act	cca	gac	tcg	acc	ttc	tca	gag	acc	ttc	aag	gaa	ggc	gtt	cag	672
Arg	Thr	Pro	Asp	Ser	Thr	Phe	Ser	Glu	Thr	Phe	Lys	Glu	Gly	Val	Gln	
					210				215				220			
gag	gtt	ttc	ttc	ccc	tcg	gat	ctc	agt	ctg	cgg	atg	cct	ggc	atg	aat	720
Glu	Val	Phe	Phe	Pro	Ser	Asp	Leu	Ser	Leu	Arg	Met	Pro	Gly	Met	Asn	
					225				230				235			
tca	gag	gac	tat	gtt	ttt	gac	agt	gtt	tct	ggg	aac	aac	ttt	gaa	tat	768
Ser	Glu	Asp	Tyr	Val	Phe	Asp	Ser	Val	Ser	Gly	Asn	Asn	Phe	Glu	Tyr	
					240				245				250			
acc	cta	gaa	gct	tca	aaa	tca	ctt	cga	cag	aag	cca	gga	gac	agt	acc	816
Thr	Leu	Glu	Ala	Ser	Lys	Ser	Leu	Arg	Gln	Lys	Pro	Gly	Asp	Ser	Thr	
					255				260			265			270	
atg	acg	tac	ctg	aac	aaa	ggc	cag	ttc	tat	ccc	atc	acc	ttg	aag	gag	864
Met	Thr	Tyr	Leu	Asn	Lys	Gly	Gln	Phe	Tyr	Pro	Ile	Thr	Leu	Lys	Glu	
					275				280				285			
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Val	Ser	Ser	Ser	Glu	Gly	Ile	His	His	Pro	Ile	Ser	Lys	Val	Arg	Ser	
					290				295				300			
gtg	atc	atg	gtg	gtt	ttt	gct	gaa	gac	aaa	agc	aga	gaa	gat	cag	tta	960
Val	Ile	Met	Val	Val	Phe	Ala	Glu	Asp	Lys	Ser	Arg	Glu	Asp	Gln	Leu	
					305				310				315			
agg	cat	tgg	aag	tac	tgg	cac	tcc	cg	cag	cac	acc	gct	aaa	caa	aga	1008
Arg	His	Trp	Lys	Tyr	Trp	His	Ser	Arg	Gln	His	Thr	Ala	Lys	Gln	Arg	
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tgc att gac ata gct gac tat awa gaa agc ttc aac act atc agt aac Cys Ile Asp Ile Ala Asp Tyr Xaa Glu Ser Phe Asn Thr Ile Ser Asn 335 340 345 350	1056
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gat gaa gca aag gtt ttc atc tct gtg aac tgc tta agc aca gat ttc Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe 370 375 380	1152
tct tcc cag aag gga gtg aag ggg ttg cct ctt aac att caa gtt gat Ser Ser Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val Asp 385 390 395	1200
acc tat agt tac aac aac cgc agc aac aag cct gtg cac cgg gcc tac Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr 400 405 410	1248
tgc cag atc aag gtc ttc tgt gac aag gga gct gag cgg aaa atc agg Cys Gln Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg 415 420 425 430	1296
gat gaa gaa cga aag caa agc aaa aga aaa gtt tct gat gtt aaa gtg Asp Glu Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val 435 440 445	1344
cca ctg ctt ccc tct cac aag cga atg gat atc aca gtt ttc aaa ccc Pro Leu Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys Pro 450 455 460	1392
ttc att gat ctc gat act cag cct gtc ctc ttc att cct gac gtg cac Phe Ile Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His 465 470 475	1440
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gaa ttg gag ggt gaa ggc tct gtc ttg aaa agg ggg ccg tac ggc aca Glu Leu Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr 495 500 505 510	1536
gaa gat gac ttt gct gtc cct cct tct acc aag ctg gcc cgg ata gaa Glu Asp Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu 515 520 525	1584
gaa cca aag aga gtg ctg ctc tac gtt cga aag gag tca gaa gaa gtc Glu Pro Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val 530 535 540	1632
ttt gat gcc ctg atg ctc aaa acc cca tct ttg aag ggc ttg atg gaa Phe Asp Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu 545 550 555	1680
gct atc tca gac aaa tac gat gtt ccc cat gac aag att ggg aaa ata Ala Ile Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile 560 565 570	1728
ttc aag aag tgt aaa aag ggg atc ctg gtg aac atg gac gac aac att Phe Lys Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile 575 580 585 590	1776

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gtg aag cat tac tcc aat gag gac acc ttc cag ctg cag att gaa gaa	1824
Val Lys His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu	
595 600 605	
gcc ggg ggg tct tac aag ctc acc ctg acg gag atc taaaggcctg	1870
Ala Gly Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile	
610 615	
cgggccacag ctccccagga gttcagtgc a ggtgtttcta gatcttacgg tttggcaact	1930
gcaggttaacc ccagtcagcc atgtcgccag cacaggtcta tgtcgaggga atgggttcct	1990
tgcaggttgg aggccgggct gcatctggct tggtggtagc atttaatcta ttgcattgg	2050
gtttttcaga tgaaagagaa atccatatac cattatgtt gaatttcctg atatatacag	2110
gatttaaagt gaaaactta ttccaagagt taacagagtc tctggaaagc tttaggacat	2170
ctgctacgtt atttatcaa atattggat ctctgccttg tgcctacagt gtcgtggcc	2230
tgctcgctag cagaagtcag aaaaggcgat aggcttgct ttaaggattt cgtgcccttg	2290
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gggagccctc t	2361

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<223> The 'xaa' at location 342 stands for Lys, or Ile.

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Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met
35 40 45

Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Leu Gly Leu Leu
50 55 60

Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Thr Ala Lys
65 70 75 80

Pro Glu Val Glu His Pro Glu Pro Asp His Ser Lys Arg Asn Ser Ile
85 90 95

DAVI251.001APC_sequence listing.TXT

Pro Ile Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val
100 105 110

Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Gly Asn
115 120 125

Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Ser Asp Thr Thr
130 135 140

Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu
145 150 155 160

Thr Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His
165 170 175

Pro Glu Pro Thr Glu Arg Val Val Val Phe Asp Arg Asn Leu Asn Thr
180 185 190

Asp Gln Phe Ser Ser Gly Ala Gln Ala Pro Asn Ala Gln Arg Arg Thr
195 200 205

Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val
210 215 220

Phe Phe Pro Ser Asp Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu
225 230 235 240

Asp Tyr Val Phe Asp Ser Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu
245 250 255

Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr Met Thr
260 265 270

Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu Val Ser
275 280 285

Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile
290 295 300

Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His
305 310 315 320

Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile
325 330 335

Asp Ile Ala Asp Tyr Xaa Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu
340 345 350

DAVI251.001APC_sequence listing.TXT

Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu
355 360 365

Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser
370 375 380

Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val Asp Thr Tyr
385 390 395 400

Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln
405 410 415

Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu
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Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Pro Leu
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Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys Pro Phe Ile
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Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Ala
465 470 475 480

Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser Glu Glu Leu
485 490 495

Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr Glu Asp
500 505 510

Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu Glu Pro
515 520 525

Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp
530 535 540

Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile
545 550 555 560

Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys
565 570 575

Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys
580 585 590

His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly

Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile
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 Val Pro Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr
 15 20 25 30
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 Ser Glu Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala
 35 40 45
 gcc acc aag gcc atg atg agc att aat ggt gat gag gac agt gct gct 252
 Ala Thr Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala
 50 55 60
 gcc ctc ggc ctg ctc tat gac tac tac aag gtt cct cga gac aag agg 300
 Ala Leu Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg
 65 70 75
 ctg ctg tct gta agc aaa gca agt gac agc caa gaa gac cag gag aaa 348
 Leu Leu Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Glu Lys
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 Arg Asn Cys Leu Gly Thr Ser Glu Ala Gln Ser Asn Leu Ser Gly Gly
 95 100 105 110
 gaa aac cga gtg caa gtc cta aag act gtt cca gtg aac ctt tcc cta 444
 Glu Asn Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Ser Leu
 115 120 125
 aat caa gat cac ctg gag aat tcc aag cgg gaa cag tac agc atc agc 492
 Asn Gln Asp His Leu Glu Asn Ser Lys Arg Glu Gln Tyr Ser Ile Ser
 130 135 140
 ttc ccc gag agc tct gcc atc atc ccg gtg tcg gga atc acg gtg gtg 540
 Phe Pro Glu Ser Ser Ala Ile Ile Pro Val Ser Gly Ile Thr Val Val
 145 150 155
 aaa gct gaa gat ttc aca cca gtt ttc atg gcc cca cct gtg cac tat 588
 Lys Ala Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr
 160 165 170

DAVI251.001APC_sequence listing.TXT

ccc	cg	g	g	g	at	g	g	g	aa	g	ag	ca	ca	gt	gt	at	tc	tt	g	aa	c	ag	ac	636	
Pro	Arg	Gly	Asp	Gly	Glu	Glu	Gln	Arg	Val	Val	Val	Ile	Phe	Glu	Gln	Thr									
175					180							185												190	
cag	ta	g	ac	gt	cc	tc	ct	g	cc	ac	ca	ca	ag	g	cc	ta	tc	tt	aa	g	ac	684			
Gln	Tyr	Asp	Val	Pro	Ser	Leu	Ala	Thr	His	Ser	Ala	Tyr	Leu	Lys	Asp										
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gac	ca	cg	ac	ac	cc	g	ac	ac	ca	ta	ag	g	ag	ac	tt	a	ag	g	ac	732					
Asp	Gln	Arg	Ser	Thr	Pro	Asp	Ser	Thr	Tyr	Ser	Glu	Ser	Phe	Lys	Asp										
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gca	g	cc	ac	ga	aa	tt	cg	ag	gt	g	ct	t	ca	gt	gg	g	ct	ga	ga	ga	ta	780			
Ala	Ala	Thr	Glu	Lys	Phe	Arg	Ser	Ala	Ser	Ala	Ser	Val	Gly	Ala	Glu	Glu	Tyr								
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atg	ta	ta	ga	ac	ta	ag	g	gc	ac	tt	ca	ta	ac	cc	ct	ga	aa	gc	828						
Met	Tyr	Asp	Gln	Thr	Ser	Ser	Gly	Thr	Phe	Gln	Tyr	Thr	Leu	Glu	Ala										
					240							245												250	
acc	aa	t	ct	ct	cgt	c	ag	a	ag	c	gg	g	ag	gg	cc	at	g	ac	ta	ct	876				
Thr	Lys	Ser	Leu	Arg	Gln	Lys	Gln	Gly	Glu	Gly	Gly	Pro	Met	Thr	Tyr	Leu									
					255							260												270	
aac	aa	g	ga	c	tt	ta	g	cc	at	ac	ct	ac	ga	ac	gg	ga	ac	aa	924						
Asn	Lys	Gly	Gln	Phe	Tyr	Ala	Ile	Thr	Leu	Ser	Glu	Thr	Gly	Asp	Asn										
					275							280												285	
aaa	tg	tc	cg	ca	cc	at	ac	g	tc	ag	ag	gt	gt	gt	at	tg	gt	972							
Lys	Cys	Phe	Arg	His	Pro	Ile	Ser	Lys	Val	Arg	Ser	Val	Val	Val	Met	Val									
					290							295												300	
gtc	tt	ag	ga	ga	aa	aa	ag	ga	ta	ca	ct	aa	ta	ca	tt	gg	aa	1020							
Val	Phe	Ser	Glu	Asp	Lys	Asn	Arg	Asp	Glu	Gln	Leu	Lys	Tyr	Trp	Lys										
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Tyr	Trp	His	Ser	Arg	Gln	His	Thr	Ala	Lys	Gln	Arg	Val	Leu	Asp	Ile										
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gcc	ga	ta	aa	ga	ag	tc	tt	aa	at	ac	tt	gg	aa	ac	at	ga	ga	at	1116						
Ala	Asp	Tyr	Lys	Glu	Ser	Phe	Asn	Thr	Ile	Gly	Asn	Ile	Glu	Glu	Ile										
					335							340												350	
gca	ta	ta	g	ct	tcc	ttt	ac	tg	g	ac	gt	aa	ta	ga	ga	gc	aa	1164							
Ala	Tyr	Asn	Ala	Val	Ser	Phe	Thr	Trp	Asp	Val	Asn	Glu	Glu	Ala	Lys										
					355							360												365	
att	tt	at	ac	cc	gt	aa	at	tg	tt	ag	ca	ga	tt	tc	tc	ca	aa	aa	1212						
Ile	Phe	Ile	Thr	Val	Asn	Cys	Leu	Ser	Thr	Asp	Phe	Ser	Ser	Gl	in	Lys									
					370							375												380	
ggg	gt	aa	g	ga	ct	c	tt	tg	at	c	at	g	ac	ca	ta	ac	tg	ta	1260						
Gly	Val	Lys	Gly	Leu	Pro	Leu	Met	Ile	Gln	Ile	Asp	Thr	Tyr	Ser	Tyr										
					385							390												395	
aac	aa	cgt	ag	ac	aa	aa	cc	at	ca	ag	g	ct	ta	tc	ca	tg	ca	at	1308						
Asn	Asn	Arg	Ser	Asn	Lys	Pro	Ile	His	Arg	Ala	Tyr	Cys	Gln	Ile	Lys										
					400							405												410	
gtc	tt	tc	t	gt	g	aa	aa	g	ca	g	aa	aa	at	cg	ga	ga	gg	cg	1356						
Val	Phe	Cys	Asp	Lys	Gly	Ala	Glu	Arg	Lys	Ile	Arg	Asp	Glu	Glu	Arg										

DAVI251.001APC_sequence listing.TXT

415	420	425	430
aag cag aac agg aag aaa ggg aaa ggc cag gcc tcc caa act caa tgc Lys Gln Asn Arg Lys Lys Gly Lys Gly Gln Ala Ser Gln Thr Gln Cys 435 440 445			1404
aac agc tcc tct gat ggg aag ttg gct gcc ata cct tta cag aag aag Asn Ser Ser Ser Asp Gly Lys Leu Ala Ala Ile Pro Leu Gln Lys Lys 450 455 460			1452
agt gac atc acc tac ttc aaa acc atg cct gat ctc cac tca cag cca Ser Asp Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro 465 470 475			1500
gtt ctc ttc ata cct gat gtt cac ttt gca aac ctg cag agg acc gga Val Leu Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly 480 485 490			1548
cag gtg tat tac aac acg gat gat gaa cga gaa ggt ggc agt gtc ctt Gln Val Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Gly Ser Val Leu 495 500 505 510			1596
gtt aaa cgg atg ttc cgg ccc atg gaa gag gag ttt ggt cca gtg cct Val Lys Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Val Pro 515 520 525			1644
tca aag cag atg aaa gaa gaa ggg aca aag cga gtg ctc ttg tac gtg Ser Lys Gln Met Lys Glu Glu Gly Thr Lys Arg Val Leu Leu Tyr Val 530 535 540			1692
agg aag gag act gac gat gtg ttc gat gca ttg atg ttg aag tct ccc Arg Lys Glu Thr Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro 545 550 555			1740
aca gtg aag ggc ctg atg gaa gcg ata tct gag aaa tat ggg ctg ccc Thr Val Lys Gly Leu Met Glu Ala Ile Ser Glu Lys Tyr Gly Leu Pro 560 565 570			1788
gtg gag aag ata gca aag ctt tac aag aaa agc aaa aaa ggc atc ttg Val Glu Lys Ile Ala Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu 575 580 585 590			1836
gtg aac atg gat gac aac atc atc gag cac tac tcg aac gag gac acc Val Asn Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr 595 600 605			1884
ttc atc ctc aac atg gag agc atg gtg gag ggc ttc aag gtc acg ctc Phe Ile Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Val Thr Leu 610 615 620			1932
atg gaa atc tagccctggg tttggcatcc gctttggctg gagctctcag Met Glu Ile 625			1981
tgcgttcctc cctgagagag acagaagccc cagccccaga acctggagac ccatctcccc catctcacaa ctgctgttac aagaccgtgc tggggagtgg ggcaaggac aggccccact gtcggtgtgc ttggccatc cactggcacc taccacggag ctgaagcctg agcccccctag gaaggtgcct taggcctgtt ggattcctat ttattgcccc cctttcctg gagcccaggt ccaggccccgc caggactctg caggtcactg cttagctccag atgagaccgt ccagcgttcc			2041 2101 2161 2221 2281

DAVI251.001APC_sequence listing.TXT

cccttcaaga gaaacactca tcccaacag cctaaaaat tcccatccct tctctctcac	2341
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 agtgcacat cccttccat ccattccct ctgcattcctc ggagcaccgg agtttgcctt 4321
 ttagtgcgtcc gctgtgtatg ttagctgaac tttgatgagc aaaatttcct gagcgaac 4381
 ctccaaagag ataggaaaac ttgcgcctc ttctttttg tcccttaatc aaactcaaata 4441
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Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr Ser Glu
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Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr
 35 40 45

Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu
 50 55 60

Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg Leu Leu
 65 70 75 80

Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Glu Lys Arg Asn
 85 90 95

Cys Leu Gly Thr Ser Glu Ala Gln Ser Asn Leu Ser Gly Gly Glu Asn
 100 105 110

Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Ser Leu Asn Gln
 115 120 125

Asp His Leu Glu Asn Ser Lys Arg Glu Gln Tyr Ser Ile Ser Phe Pro
 130 135 140

Glu Ser Ser Ala Ile Ile Pro Val Ser Gly Ile Thr Val Val Lys Ala
 145 150 155 160

Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr Pro Arg

DAVI251.001APC_sequence listing.TXT
165 170 175

Gly Asp Gly Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr Gln Tyr
180 185 190

Asp Val Pro Ser Leu Ala Thr His Ser Ala Tyr Leu Lys Asp Asp Gln
195 200 205

Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp Ala Ala
210 215 220

Thr Glu Lys Phe Arg Ser Ala Ser Val Gly Ala Glu Glu Tyr Met Tyr
225 230 235 240

Asp Gln Thr Ser Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala Thr Lys
245 250 255

Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu Asn Lys
260 265 270

Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn Lys Cys
275 280 285

Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val Val Phe
290 295 300

Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys Tyr Trp
305 310 315 320

His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile Ala Asp
325 330 335

Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile Ala Tyr
340 345 350

Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys Ile Phe
355 360 365

Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val
370 375 380

Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr Asn Asn
385 390 395 400

Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys Val Phe
405 410 415

DAVI251.001APC_sequence listing.TXT
Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln
420 425 430

Asn Arg Lys Lys Gly Lys Gly Gln Ala Ser Gln Thr Gln Cys Asn Ser
435 440 445

Ser Ser Asp Gly Lys Leu Ala Ala Ile Pro Leu Gln Lys Lys Ser Asp
450 455 460

Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro Val Leu
465 470 475 480

Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly Gln Val
485 490 495

Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Gly Ser Val Leu Val Lys
500 505 510

Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Val Pro Ser Lys
515 520 525

Gln Met Lys Glu Glu Gly Thr Lys Arg Val Leu Leu Tyr Val Arg Lys
530 535 540

Glu Thr Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro Thr Val
545 550 555 560

Lys Gly Leu Met Glu Ala Ile Ser Glu Lys Tyr Gly Leu Pro Val Glu
565 570 575

Lys Ile Ala Lys Leu Tyr Lys Ser Lys Lys Gly Ile Leu Val Asn
580 585 590

Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr Phe Ile
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Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Val Thr Leu Met Glu
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Ile
625

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<222> 172

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Asn Ser Ile Leu Pro Ile Phe Leu Phe Arg Ser Val Arg Leu Leu Lys	
5 10 15	

aac gac cca gtc aac ttg cag aaa ttc tct tac act agt gag gat gag	151
Asn Asp Pro Val Asn Leu Gln Lys Phe Ser Tyr Thr Ser Glu Asp Glu	
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gcc tgg aag acg tac cta gaa aac ccg ttg aca gct gcc aca aag gcc	199
Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala	
40 45 50	

atg atg aga gtc aat gga gat gat gac agt gtt gcg gcc ttg agc ttc	247
Met Met Arg Val Asn Gly Asp Asp Asp Ser Val Ala Ala Leu Ser Phe	
55 60 65	

ctc tat gat tac tac atg ggt ccc aag gag aag cgg ata ttg tcc tcc	295
Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile Leu Ser Ser	
70 75 80	

agc act ggg ggc agg aat gac caa gga aag agg tac tac cat ggc atg	343
Ser Thr Gly Gly Arg Asn Asp Gln Gly Lys Arg Tyr Tyr His Gly Met	
85 90 95	

gaa tat gag acg gac ctc act ccc ctt gaa agc ccc aca cac ctc atg	391
Glu Tyr Glu Thr Asp Leu Thr Pro Leu Glu Ser Pro Thr His Leu Met	
100 105 110 115	

aaa ytc ctg aca gag aac gtg tct gga acc cca gag tac cca gat ttg	439
Lys Xaa Leu Thr Glu Asn Val Ser Gly Thr Pro Glu Tyr Pro Asp Leu	
120 125 130	

ctc aag aag aat aac ctg atg agc ttg gag ggg gcc ttg ccc acc cct	487
Leu Lys Lys Asn Asn Leu Met Ser Leu Glu Gly Ala Leu Pro Thr Pro	
135 140 145	

ggc aag gca gct ccc ctc cct gca ggc ccc agc aag ctg gag gcc ggc	535
Gly Lys Ala Ala Pro Leu Pro Ala Gly Pro Ser Lys Leu Glu Ala Gly	
150 155 160	

tct gtg gac agc tac ctg tta ccc acy act gat atg tat gat aat ggc	583
Ser Val Asp Ser Tyr Leu Leu Pro Xaa Thr Asp Met Tyr Asp Asn Gly	
165 170 175	

DAVI251.001APC_sequence listing.TXT

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180				185					190						195	
cgc	tgg	cag	cca	gac	agc	acc	ttc	aaa	gat	gac	cca	cag	gag	tcg	atg	679
Arg	Trp	Gln	Pro	Asp	Ser	Thr	Phe	Lys	Asp	Asp	Pro	Gln	Glu	Ser	Met	
				200					205						210	
ctc	ttc	cca	gat	atc	ctg	aaa	acc	tcc	ccg	gaa	ccc	cca	tgt	cca	gag	727
Leu	Phe	Pro	Asp	Ile	Leu	Lys	Thr	Ser	Pro	Glu	Pro	Pro	Cys	Pro	Glu	
				215				220							225	
gac	tac	ccc	agc	ctc	aaa	agt	gac	ttt	gaa	tac	acc	ctg	ggc	tcc	ccc	775
Asp	Tyr	Pro	Ser	Leu	Lys	Ser	Asp	Phe	Glu	Tyr	Thr	Leu	Gly	Ser	Pro	
				230			235				240					
aaa	gcc	atc	cac	atc	aag	tca	ggc	gag	tca	ccc	atg	gcc	tac	ctc	aac	823
Lys	Ala	Ile	His	Ile	Lys	Ser	Gly	Glu	Ser	Pro	Met	Ala	Tyr	Leu	Asn	
				245			250				255					
aaa	ggc	cag	ttc	tac	ccc	gtc	acc	ctg	cg	acc	cca	gca	ggt	ggc	aaa	871
Lys	Gly	Gln	Phe	Tyr	Pro	Val	Thr	Leu	Arg	Thr	Pro	Ala	Gly	Gly	Lys	
				260			265			270					275	
ggc	ctt	gcc	ttg	tcc	tcc	aac	aaa	gtc	aag	agt	gtg	gtg	atg	gtt	gtc	919
Gly	Leu	Ala	Leu	Ser	Ser	Asn	Lys	Val	Lys	Ser	Val	Val	Met	Val	Val	
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Phe	Asp	Asn	Glu	Lys	Val	Pro	Val	Glu	Gln	Leu	Arg	Phe	Trp	Lys	His	
				295			300				305					
tgg	cat	tcc	cg	caa	ccc	act	gcc	aag	cag	cg	gtc	att	gac	gtg	gct	1015
Trp	His	Ser	Arg	Gln	Pro	Thr	Ala	Lys	Gln	Arg	Val	Ile	Asp	Val	Ala	
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gac	tgc	aaa	gaa	aac	ttc	aac	act	gtg	gag	cac	att	gag	gag	gtg	gcc	1063
Asp	Cys	Lys	Glu	Asn	Phe	Asn	Thr	Val	Glu	His	Ile	Glu	Glu	Val	Ala	
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Tyr	Asn	Ala	Leu	Ser	Phe	Val	Trp	Asn	Val	Asn	Glu	Glu	Ala	Lys	Val	
				340			345			350				355		
ttc	atc	ggc	gta	aac	tgt	ctg	agc	aca	gac	ttt	tcc	tca	caa	aag	ggg	1159
Phe	Ile	Gly	Val	Asn	Cys	Leu	Ser	Thr	Asp	Phe	Ser	Ser	Gln	Lys	Gly	
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gtg	aag	ggt	gtc	ccc	ctg	aac	ctg	cag	att	gac	acc	tat	gac	tgt	gac	1207
Val	Lys	Gly	Val	Pro	Leu	Asn	Leu	Gln	Ile	Asp	Thr	Tyr	Asp	Cys	Gly	
				375			380				385					
ttg	ggc	act	gag	cg	ctg	gta	cac	cgt	gct	gtc	tgc	cag	atc	aag	atc	1255
Leu	Gly	Thr	Glu	Arg	Leu	Val	His	Arg	Ala	Val	Cys	Gln	Ile	Lys	Ile	
				390			395				400					
ttc	tgt	gac	aag	gga	gct	gag	agg	aag	atg	cgc	gat	gac	gag	cg	aag	1303
Phe	Cys	Asp	Lys	Gly	Ala	Glu	Arg	Lys	Met	Arg	Asp	Asp	Glu	Arg	Lys	
				405			410				415					
cag	ttc	cg	agg	aag	gtc	aag	tgc	cct	gac	tcc	agc	aac	agt	ggc	gtc	1351
Gln	Phe	Arg	Arg	Lys	Val	Lys	Cys	Pro	Asp	Ser	Ser	Asn	Ser	Gly	Val	

DAVI251.001APC_sequence listing.TXT

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Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr Thr Tyr Leu				
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cgg cca gag act gac ctg gag acg cca ccc gtg ctg ttc atc ccc aat				1447
Arg Pro Glu Thr Asp Leu Glu Thr Pro Pro Val Leu Phe Ile Pro Asn				
455	460	465		
gtg cac ttc tcc agc ctg cag cgc tct gga ggg gca gcc ccc tcg gca				1495
Val His Phe Ser Ser Leu Gln Arg Ser Gly Gly Ala Ala Pro Ser Ala				
470	475	480		
gga ccc agc agc tcc aac agg ctg cct ctg aag cgt acc tgc tcg ccc				1543
Gly Pro Ser Ser Asn Arg Leu Pro Leu Lys Arg Thr Cys Ser Pro				
485	490	495		
ttc act gag gag ttt gag cct ctg ccc tcc aag cag gcc aag gaa ggc				1591
Phe Thr Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala Lys Glu Gly				
500	505	510	515	
gac ctt cag aga gtt ctg ctg tat gtg cg agg gag act gag gag gtg				1639
Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr Glu Glu Val				
520	525	530		
ttt gac gcg ctc atg ttg aag acc cca gac ctg aag ggg ctg agg aat				1687
Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly Leu Arg Asn				
535	540	545		
gcg atc tct gag aag tat ggg ttc cct gaa gag aac att tac aaa gtc				1735
Ala Ile Ser Glu Lys Tyr Gly Phe Pro Glu Glu Asn Ile Tyr Lys Val				
550	555	560		
tac aag aaa tgc aag cga gga atc tta gtc aac atg gac aac aac atc				1783
Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp Asn Asn Ile				
565	570	575		
att cag cat tac agc aac cac gtc gcc ttc ctg ctg gac atg ggg gag				1831
Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp Met Gly Glu				
580	585	590	595	
ctg gac ggc aaa att cag atc atc ctt aag gag ctg taa				1870
Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu				
600	605			

<210> 8
<211> 607
<212> PRT
<213> HUMAN

<220>
<221> misc_feature
<222> (117)..(117)
<223> The 'Xaa' at location 117 stands for Leu, or Phe.

<220>
<221> misc_feature
<222> (172)..(172)
<223> The 'Xaa' at location 172 stands for Thr.

<400> 8

DAVI251.001APC_sequence listing.TXT

Met Trp Met Asn Ser Ile Leu Pro Ile Phe Leu Phe Arg Ser Val Arg
1 5 10 15

Leu Leu Lys Asn Asp Pro Val Asn Leu Gln Lys Phe Ser Tyr Thr Ser
20 25 30

Glu Asp Glu Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala
35 40 45

Thr Lys Ala Met Met Arg Val Asn Gly Asp Asp Asp Ser Val Ala Ala
50 55 60

Leu Ser Phe Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile
65 70 75 80

Leu Ser Ser Ser Thr Gly Gly Arg Asn Asp Gln Gly Lys Arg Tyr Tyr
85 90 95

His Gly Met Glu Tyr Glu Thr Asp Leu Thr Pro Leu Glu Ser Pro Thr
100 105 110

His Leu Met Lys Xaa Leu Thr Glu Asn Val Ser Gly Thr Pro Glu Tyr
115 120 125

Pro Asp Leu Leu Lys Lys Asn Asn Leu Met Ser Leu Glu Gly Ala Leu
130 135 140

Pro Thr Pro Gly Lys Ala Ala Pro Leu Pro Ala Gly Pro Ser Lys Leu
145 150 155 160

Glu Ala Gly Ser Val Asp Ser Tyr Leu Leu Pro Xaa Thr Asp Met Tyr
165 170 175

Asp Asn Gly Ser Leu Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro
180 185 190

Pro Thr Gln Arg Trp Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln
195 200 205

Glu Ser Met Leu Phe Pro Asp Ile Leu Lys Thr Ser Pro Glu Pro Pro
210 215 220

Cys Pro Glu Asp Tyr Pro Ser Leu Lys Ser Asp Phe Glu Tyr Thr Leu
225 230 235 240

Gly Ser Pro Lys Ala Ile His Ile Lys Ser Gly Glu Ser Pro Met Ala
245 250 255

DAVI251.001APC_sequence listing.TXT

Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala
260 265 270

Gly Gly Lys Gly Leu Ala Leu Ser Ser Asn Lys Val Lys Ser Val Val
275 280 285

Met Val Val Phe Asp Asn Glu Lys Val Pro Val Glu Gln Leu Arg Phe
290 295 300

Trp Lys His Trp His Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile
305 310 315 320

Asp Val Ala Asp Cys Lys Glu Asn Phe Asn Thr Val Glu His Ile Glu
325 330 335

Glu Val Ala Tyr Asn Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu
340 345 350

Ala Lys Val Phe Ile Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser
355 360 365

Gln Lys Gly Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr
370 375 380

Asp Cys Gly Leu Gly Thr Glu Arg Leu Val His Arg Ala Val Cys Gln
385 390 395 400

Ile Lys Ile Phe Cys Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp
405 410 415

Glu Arg Lys Gln Phe Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn
420 425 430

Ser Gly Val Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr
435 440 445

Thr Tyr Leu Arg Pro Glu Thr Asp Leu Glu Thr Pro Pro Val Leu Phe
450 455 460

Ile Pro Asn Val His Phe Ser Ser Leu Gln Arg Ser Gly Gly Ala Ala
465 470 475 480

Pro Ser Ala Gly Pro Ser Ser Ser Asn Arg Leu Pro Leu Lys Arg Thr
485 490 495

Cys Ser Pro Phe Thr Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala

500 DAVI251.001APC_sequence listing.TXT
 505
 510

Lys Glu Gly Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr
 515 520 525

Glu Glu Val Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly
 530 535 540

Leu Arg Asn Ala Ile Ser Glu Lys Tyr Gly Phe Pro Glu Glu Asn Ile
 545 550 555 560

Tyr Lys Val Tyr Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp
 565 570 575

Asn Asn Ile Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp
 580 585 590

Met Gly Glu Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu
 595 600 605

<210> 9
 <211> 3113
 <212> DNA
 <213> MURINE

<220>
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 <222> (2634)..(2634)
 <223> n = any nucleotide

<220>
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 <222> (2968)..(2968)
 <223> n = any nucleotide

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ctaaacagca taccaaatgt gacggagcag cccctcattt ctgctggaga aaacagggta	120
caagtgctga aaaacgtgcc cttcaacatc gtcctcccc atagcaacca gctggcatt	180
gataagagag gccatctgac agctcccgat acaacagtca ctgtctccat agcgaccatg	240
cctacccact ccatcaagac agaaatccag ccgcacggct ttgctgtggg aatccctcca	300
gccgtgtacc actctgagcc caccgaacgc gtgggtggtt ttgaccggag cctcagcact	360
gatcagttca gctctggcac tcagcccccc aatgctcagc ggaggactcc agactccacc	420
ttctccgaga cttcaaggaa gggcgttcag gaggtttct tccctcgga actcagcctt	480
cggatgccgg gcatgaattc agaggactat gtcttgaca atgtttctgg gaacaacttt	540

DAVI251.001APC_sequence listing.TXT

gagtataccc	tggaagcctc	caagtcactg	cggcagaagc	aaggggacag	cactatgaca	600
tacctgaata	aaggccagtt	ctatcctgtc	accttaaagg	aaggaagcag	aatgaaggg	660
attcaccacc	ctatcagcaa	agttcgaagt	gtgatcatgg	tggttttgc	tgaagacaaa	720
agcagagaag	accagctgag	acactggaag	tactggcact	cccgtagca	cacggccaaa	780
cagaggtgca	ttgacattgc	tgactacaaa	gaaagttca	acactatcag	caacattgag	840
gagatagctt	ataacgccc	ttccttcacg	tgggacatca	atgatgaggc	aaaggtcttc	900
atctctgtga	actgcttgag	cacagatttc	tcttctcaga	agggtgtgaa	gggcttgcca	960
ctcaacattc	aatcgacac	atacagctat	aacaaccgca	gcaacaagcc	ggttcaccgg	1020
gcctactgcc	agataaaaggt	cttctgcgac	aaggagctg	aaaggaaaat	tcgggatgaa	1080
gaacgaaaac	agagcaagag	aaaagtgtct	gacgttaaag	tgcagctgct	tccctcacac	1140
aaacggacag	acatcacagt	gttcaagccc	ttcctggacc	tcgacactca	gcctgtcctc	1200
ttcattccgg	acgtgcattt	taccaacctg	cagcggggca	gtcatgttct	ttccctcccc	1260
tctgaagaac	tggaaggtga	aggctctgtc	ttgaaaagag	ggccattcgg	aaccgaagat	1320
gactttggag	ttcctccctcc	tgctaagctg	actcggacag	aagaacccaa	gagagtgctg	1380
ctctatgtcc	gaaaggaatc	agaagaagtc	ttcgacgccc	tgtatgctcaa	gacgcccgtct	1440
ttgaagggccc	tgatggaggc	aatttcagac	aagtatgatg	tccccatga	caagattggg	1500
aaaatattta	agaagtgcaa	aaaagggatc	ctcgtgaaca	tggacgacaa	cattgtgaag	1560
cactactcca	atgaggacac	cttccagctg	cagatagagg	aagccggcgg	ctcgtacaag	1620
ctcacccctga	cagagattt	aaggggcagg	ggtggggggc	gctcggctcc	caggcgtggg	1680
aattcagtga	aagtgttcca	gctgagaagc	ccaggcacct	accctgcaga	accttaaata	1740
tcagggaaagg	aacctttcac	gttagaaatg	gcgctgtgta	taccgtgctg	tgttgatgtt	1800
ttcttttggaa	tagaaatcca	tgtgttgttt	tgttgttgtt	gttgaattt	ctgatgtgct	1860
tagaaagcga	agcatgagaa	ctttgtaccg	gatctaagag	accatggac	cgtttggggtt	1920
acctgctcca	ctacctgtca	aagtctgcct	gtgtccataa	gagtggtggg	ctactggctg	1980
gcgagagagg	ggaaggcagt	agcttgtctt	tgaggcttt	gtgttctcgc	ctgacctcag	2040
tctaactctg	actgccttga	ggagtgggcc	cagccctcag	caataaaggg	ctaagccttc	2100
tccctccacc	tctcctccag	tgtttactaa	atagggtgca	ttcctggAAC	cttttcccgc	2160
aacttccctt	ggacatgtgg	actgccttc	tgatgaagaa	cttgcgtgag	tgacagtgtg	2220
aagttagctc	tgttaaagct	gcgttgtata	taagtgcata	atcttttga	aggctgcct	2280
gtaaatgtgt	acatatatgt	ctgatataaa	tatataatat	ataaatgcgg	tgtctgtgta	2340
cagatagtga	aggcgagcag	gaagatctac	cttggaaatcc	ctcttagaga	agaggttaag	2400
tttattattga	taatgtggac	caagcaggta	gaacgctgtt	ttcccaaaaaa	caagcaagtg	2460

DAVI251.001APC_sequence listing.TXT

ttcccttagca tagcaaaaag ccatctcatg tggcagagcc atctgctctt gcgaatgttg	2520
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tatgaggtgt gtgtgcaggt gtcagccaag ctgtgccat gcagagactc agcngtgtca	2640
tgagccagcg attcaaacc aaatgggccc attctacaag gccatgttcc agagcttcca	2700
agcatcagct accgtgtgt tgaactggaa ggcattcatg aatttacata actgtggcag	2760
ggaaatgttt tgcacact taaatattta agaacaaaac gaaactttac aatgttaaytt	2820
tataatgaat cctgtaacag aaatacaatt gcgggtttct ttaggttcag ggaactagaa	2880
taggtcattt gtatgagtag gattgttagc ggtatacgt rgtaaaaag tactctaatt	2940
aagtatgtga acaaaaatagc tggtttnta agatacggga tacgggtcat ataacaatat	3000
tttctatttt gtttatgaa atcagctta cttgtttaa ttgtatcatt gaacatgtgt	3060
tttaaaccaa agggattgaa ttttatatgt ctatttcaaa aaaaaaaaaaaa aaa	3113

<210> 10
 <211> 536
 <212> PRT
 <213> MURINE
 <400> 10

Met Ala Ser Leu Asp Asp Glu Leu Cys Asp Leu Asn Ser Ile Pro Asn
 1 5 10 15

Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val Gln Val
 20 25 30

Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Ser Asn Gln Leu
 35 40 45

Gly Ile Asp Lys Arg Gly His Leu Thr Ala Pro Asp Thr Thr Val Thr
 50 55 60

Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu Ile Gln
 65 70 75 80

Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His Ser Glu
 85 90 95

Pro Thr Glu Arg Val Val Val Phe Asp Arg Ser Leu Ser Thr Asp Gln
 100 105 110

Phe Ser Ser Gly Thr Gln Pro Pro Asn Ala Gln Arg Arg Thr Pro Asp
 115 120 125

DAVI251.001APC_sequence_listing.TXT
Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val Phe Phe
130 135 140

Pro Ser Glu Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu Asp Tyr
145 150 155 160

Val Phe Asp Asn Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu Glu Ala
165 170 175

Ser Lys Ser Leu Arg Gln Lys Gln Gly Asp Ser Thr Met Thr Tyr Leu
180 185 190

Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Lys Glu Gly Ser Ser Asn
195 200 205

Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile Met Val
210 215 220

Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His Trp Lys
225 230 235 240

Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile Asp Ile
245 250 255

Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu Glu Ile
260 265 270

Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu Ala Lys
275 280 285

Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys
290 295 300

Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Ile Asp Thr Tyr Ser Tyr
305 310 315 320

Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln Ile Lys
325 330 335

Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg
340 345 350

Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Gln Leu Leu Pro
355 360 365

Ser His Lys Arg Thr Asp Ile Thr Val Phe Lys Pro Phe Leu Asp Leu
370 375 380

DAVI251.001APC_sequence_listing.TXT

Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Thr Asn Leu
385 390 395 400

Gln Arg Gly Ser His Val Leu Ser Leu Pro Ser Glu Glu Leu Glu Gly
405 410 415

Glu Gly Ser Val Leu Lys Arg Gly Pro Phe Gly Thr Glu Asp Asp Phe
420 425 430

Gly Val Pro Pro Pro Ala Lys Leu Thr Arg Thr Glu Glu Pro Lys Arg
435 440 445

Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp Ala Leu
450 455 460

Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile Ser Asp
465 470 475 480

Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys Lys Cys
485 490 495

Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys His Tyr
500 505 510

Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly Gly Ser
515 520 525

Tyr Lys Leu Thr Leu Thr Glu Ile
530 535

<210> 11
<211> 3452
<212> DNA
<213> MURINE

<220>
<221> misc_feature
<222> (2973)..(2973)
<223> n = any nucleotide

<220>
<221> misc_feature
<222> (3307)..(3307)
<223> n = any nucleotide

<400> 11
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atcgggtgta ctgtcccaac ccgaaagtcc agttctgcgg cccggcagcgc gcgagcgcagc 120

DAVI251.001APC_sequence_listing.TXT

gcgatgacac aggagtacga caacaaaagg cccgtgctgg tacttcagaa tgaagccctc 180
tacccacagc ggcgctccta taccagttag gatgaagcct ggaagtcgtt cctggaaaac 240
cctctcactg cgcaaccaa agcgatgatg agcatcaacg gagacgaaga cagcgcggct 300
gctgctggcc tgctctatga ctactacaag gtccccagag agcgcggc atcagccgt 360
aagcccggagg gagagcaccc agagccagag cacagcaaaa gaaacagcat accaaatgtg 420
acggagcagc ccctcatttc tgctggagaa aacagggtac aagtgtgaa aaacgtgccc 480
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gctcccgata caacagtac tgcgtccata ggcgaccatgc ctacccactc catcaagaca 600
gaaatccagc cgacggcgtt tgctgtggg atccctccag ccgtgtacca ctctgagccc 660
accgaacgcg tggtggttt tgaccggagc ctcagcactg atcagttcag ctctggcact 720
cagccccca atgctcagcg gaggactcca gactccaccc tctccgagac cttcaaggag 780
ggcgttcagg agttttctt cccctcgaa ctcagccttc ggtatgccggg catgaattca 840
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aaaggatcc tcgtgaacat ggacgacaac attgtgaagc actactccaa tgaggacacc 1920
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aggggcaggg gtggggggcg ctcggctccc aggcgtgggaa attcagtgaa agtgttccag 2040

DAVI251.001APC_sequence listing.TXT

ctgagaagcc caggcaccta ccctgcagaa ccttaaatat cagggaaagga accttcacg	2100
taggaaatgg cgctgtgtat accgtgctgt gttgatgttt tctttggat agaaatccat	2160
gtgttgtttt gttgttgtg tttgaatttc tgatgtgctt agaaagcgaa gcatgagaac	2220
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ctgcctttct gatgaagaac ttgcgtgagt gacagtgtga agttagctct gttaaagctg	2580
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tgtatataat atataatata taaatgcggt gtctgtgtac agatagtgaa ggcgagcagg	2700
aagatctacc ttgaaatccc tcttagagaa gaggttaagt tattattgat aatgtggacc	2760
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tttatatgtc tatttcaaaa aaaaaaaaaaa aa	3452

<210> 12
 <211> 618
 <212> PRT
 <213> MURINE
 <400> 12

Met Thr Gln Glu Tyr Asp Asn Lys Arg Pro Val Leu Val Leu Gln Asn
 1 5 10 15

Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp Glu Ala
 20 25 30

DAVI251.001APC_sequence listing.TXT

Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met
35 40 45

Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Leu Gly Leu Leu
50 55 60

Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Ala Val Lys
65 70 75 80

Pro Glu Gly Glu His Pro Glu Pro Glu His Ser Lys Arg Asn Ser Ile
85 90 95

Pro Asn Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val
100 105 110

Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Ser Asn
115 120 125

Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Pro Asp Thr Thr
130 135 140

Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu
145 150 155 160

Ile Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His
165 170 175

Ser Glu Pro Thr Glu Arg Val Val Val Phe Asp Arg Ser Leu Ser Thr
180 185 190

Asp Gln Phe Ser Ser Gly Thr Gln Pro Pro Asn Ala Gln Arg Arg Thr
195 200 205

Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val
210 215 220

Phe Phe Pro Ser Glu Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu
225 230 235 240

Asp Tyr Val Phe Asp Asn Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu
245 250 255

Glu Ala Ser Lys Ser Leu Arg Gln Lys Gln Gly Asp Ser Thr Met Thr
260 265 270

Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Lys Glu Gly Ser

275

DAVI251.001APC_sequence listing.TXT

280

285

Ser Asn Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile
290 295 300

Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His
305 310 315 320

Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile
325 330 335

Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu
340 345 350

Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu
355 360 365

Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser
370 375 380

Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Ile Asp Thr Tyr
385 390 395 400

Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln
405 410 415

Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu
420 425 430

Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Gln Leu
435 440 445

Leu Pro Ser His Lys Arg Thr Asp Ile Thr Val Phe Lys Pro Phe Leu
450 455 460

Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Thr
465 470 475 480

Asn Leu Gln Arg Gly Ser His Val Leu Ser Leu Pro Ser Glu Glu Leu
485 490 495

Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Phe Gly Thr Glu Asp
500 505 510

Asp Phe Gly Val Pro Pro Pro Ala Lys Leu Thr Arg Thr Glu Glu Pro
515 520 525

DAVI251.001APC_sequence listing.TXT

Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp
 530 535 540

Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile
 545 550 555 560

Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys
 565 570 575

Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys
 580 585 590

His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly
 595 600 605

Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile
 610 615

<210> 13

<211> 2195

<212> DNA

<213> murine

<400> 13

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DAVI251.001APC_sequence listing.TXT

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ctgccagtgg	agaaaatcac	aaagctttat	aagaagagca	aaaagggcat	cctggtaac	1860
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ataggagctt	ttggtatact	cttcctggg	agagatggga	tctctgccgc	cccaggacct	2040
ggagacccac	ccatctca	cacctctcaa	gactgttaca	agactgctgg	gaaggggggc	2100
agggcccaag	gcccagtaat	ggacttcctt	caactcttcc	actgctccc	tatggagctg	2160
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<211> 625

<212> PRT

<213> murine

<400> 14

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20								25					30		

Asp	Glu	Ala	Trp	Lys	Ser	Tyr	Leu	Glu	Asn	Pro	Leu	Thr	Ala	Ala	Thr
35												45			

Lys	Ala	Met	Met	Ser	Ile	Asn	Gly	Asp	Glu	Asp	Ser	Ala	Ala	Ala	Leu
50								55				60			

DAVI251.001APC_sequence listing.TXT

Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg Leu Leu
65 70 75 80

Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Asp Lys Arg Asn
85 90 95

Cys Leu Gly Thr Ser Glu Ala Gln Ile Asn Leu Ser Gly Gly Glu Asn
100 105 110

Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Cys Leu Ser Gln
115 120 125

Asp His Met Glu Asn Ser Lys Arg Glu Gln Tyr Ser Val Ser Ile Thr
130 135 140

Glu Ser Ser Ala Val Ile Pro Val Ser Gly Ile Thr Val Val Lys Ala
145 150 155 160

Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr Pro Arg
165 170 175

Ala Asp Ser Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr Gln Tyr
180 185 190

Asp Leu Pro Ser Ile Ala Ser His Ser Ser Tyr Leu Lys Asp Asp Gln
195 200 205

Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp Gly Ala
210 215 220

Ser Glu Lys Phe Arg Ser Thr Ser Val Gly Ala Asp Glu Tyr Thr Tyr
225 230 235 240

Asp Gln Thr Gly Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala Thr Lys
245 250 255

Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu Asn Lys
260 265 270

Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn Lys Cys
275 280 285

Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val Val Phe
290 295 300

Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys Tyr Trp

DAVI251.001APC_sequence_listing.TXT
305 310 315 320

His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile Ala Asp
325 330 335

Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile Ala Tyr
340 345 350

Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys Ile Phe
355 360 365

Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val
370 375 380

Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr Asn Asn
385 390 395 400

Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys Val Phe
405 410 415

Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln
420 425 430

Asn Arg Lys Lys Gly Lys Gly Gln Ala Ser Gln Ala Gln Cys Asn Asn
435 440 445

Ser Ser Asp Gly Lys Met Ala Ala Ile Pro Leu Gln Lys Lys Ser Asp
450 455 460

Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro Val Leu
465 470 475 480

Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly Gln Val
485 490 495

Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Ser Ser Val Leu Val Lys
500 505 510

Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Thr Pro Ser Lys
515 520 525

Gln Ile Lys Glu Glu Asn Val Lys Arg Val Leu Leu Tyr Val Arg Lys
530 535 540

Glu Asn Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro Thr Val
545 550 555 560

DAVI251.001APC_sequence listing.TXT
Lys Gly Leu Met Glu Ala Leu Ser Glu Lys Tyr Gly Leu Pro Val Glu
565 570 575

Lys Ile Thr Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu Val Asn
580 585 590

Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr Phe Ile
595 600 605

Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Ile Thr Leu Met Glu
610 615 620

Ile
625

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<212> DNA
<213> murine

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<222> (200)..(2008)

<220>
<221> misc_feature
<222> (2806)..(2806)
<223> n = any nucleotide

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gaggagaatt aagagacgag tggtcagcag cgcctgcgag ccaaccagag acggatcgct 180
ggaacctcgg agaaggaag atg tcg aat gaa ctt gat ttc agg tct gtg cgg 232
Met Ser Asn Glu Leu Asp Phe Arg Ser Val Arg
1 5 10

ttg ctg aag aat gac cct gtg agc ttc cag aag ttt ccc tac agt aat 280
Leu Leu Lys Asn Asp Pro Val Ser Phe Gln Lys Phe Pro Tyr Ser Asn
15 20 25

gag gac gag gcc tgg aag aca tac ctg gag aac cct ttg acg gct gcc 328
Glu Asp Glu Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala
30 35 40

acc aaa gcc atg atg aga gtc aac ggg gac gag gag agt gtg gct gct 376
Thr Lys Ala Met Met Arg Val Asn Gly Asp Glu Glu Ser Val Ala Ala
45 50 55

ctg agc ttc ctc tac gac tac tat atg ggt ccc aag gag aag cggtata 424
Leu Ser Phe Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile
60 65 70 75

DAVI251.001APC_sequence listing.TXT													
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Leu	Ser	Ser	Ser	Thr	Gly	Gly	Arg	Asn	Asp	Gln	Gly	Lys	Lys
80													90
472													
cac	agc	atg	gac	tat	gag	ccg	gat	ctt	gcc	ccc	ctc	gag	agc
His	Ser	Met	Asp	Tyr	Glu	Pro	Asp	Leu	Ala	Pro	Leu	Glu	Ser
95								100					105
520													
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His	Leu	Met	Lys	Phe	Leu	Thr	Glu	Asn	Val	Ser	Gly	Ser	Pro
110							115				120		
568													
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Thr	Asp	Gln	Leu	Lys	Lys	Asn	Asn	Leu	Leu	Gly	Leu	Glu	Gly
125						130				135		Val	Val
616													
ccc	acc	ccc	ggc	aag	acc	aat	acc	gtc	ccc	cca	ggt	ccg	agt
Pro	Thr	Pro	Gly	Lys	Thr	Asn	Thr	Val	Pro	Pro	Gly	Pro	Ser
140						145			150				155
664													
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Glu	Ala	Ser	Ser	Met	Asp	Ser	Tyr	Leu	Leu	Pro	Ala	Ser	Asp
160						165							170
712													
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Asp	Asn	Gly	Ser	Leu	Asn	Ser	Leu	Phe	Glu	Ser	Ile	His	Gly
175						180					185		Val
760													
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Pro	Thr	Gln	Arg	Trp	Gln	Pro	Asp	Ser	Thr	Phe	Lys	Asp	Asp
190						195				200			Pro
808													
gag	tct	ctg	ctc	ttc	cct	gat	att	ctg	aag	aca	tcc	ccg	gac
Glu	Ser	Leu	Leu	Phe	Pro	Asp	Ile	Leu	Lys	Thr	Ser	Pro	Asp
205						210				215			Pro
856													
tgc	cca	gag	gat	tat	cca	ggc	ctc	aag	agt	gac	ttt	gaa	tac
Cys	Pro	Glu	Asp	Tyr	Pro	Gly	Leu	Lys	Ser	Asp	Phe	Glu	Tyr
220						225				230			235
904													
ggc	tcc	ccc	aaa	gcc	att	cac	atc	aaa	gca	ggg	gag	tca	ccc
Gly	Ser	Pro	Lys	Ala	Ile	His	Ile	Lys	Ala	Gly	Glü	Ser	Pro
240						245				250			Met
952													
tac	ctc	aac	aag	ggt	cag	tcc	tac	ccc	gtc	acc	cta	cgc	acc
Tyr	Leu	Asn	Lys	Gly	Gln	Phe	Tyr	Pro	Val	Thr	Leu	Arg	Thr
255						260				265			Pro
1000													
gga	ggg	aaa	ggc	ctc	gct	ctg	tcc	tcc	agc	aaa	gtc	aag	agc
Gly	Gly	Lys	Gly	Leu	Ala	Leu	Ser	Ser	Ser	Lys	Val	Lys	Ser
270						275				280			Val
1048													
atg	gtc	gtg	ttc	gat	aat	gac	aag	gtc	ccc	gtg	gag	cag	ctg
Met	Val	Val	Phe	Asp	Asn	Asp	Lys	Val	Pro	Val	Glü	Gln	Leu
285						290				295			Arg
1096													
tgg	agg	cac	tgg	cat	tcc	cg	cag	ccc	acc	gcc	aag	cag	cgc
Trp	Arg	His	Trp	His	Ser	Arg	Gln	Pro	Thr	Ala	Lys	Gln	Arg
300						305				310			Val
1144													
gac	gta	gct	gac	tgt	aag	gaa	aac	tcc	aac	acg	gtc	cag	cac
Asp	Val	Ala	Asp	Cys	Lys	Glu	Asn	Phe	Asn	Thr	Val	Gln	His
320						325				330			Ile
1192													

DAVI251.001APC_sequence listing.TXT

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gcc aag gtg ttt atc ggt gtc aac tgt ctg agc aca gac ttc tcc tcg	1288
Ala Lys Val Phe Ile Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser	
350 355 360	
cag aag gga gtg aag ggt gtc ccc ctg aac ttg caa att gac acc tat	1336
Gln Lys Gly Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr	
365 370 375	
gac tgt gga gca ggc act gag cgc ctg gta cac cgt gct gtc tgc cag	1384
Asp Cys Gly Ala Gly Thr Glu Arg Leu Val His Arg Ala Val Cys Gln	
380 385 390 395	
atc aag atc ttc tgt gat aag gga gct gag agg aag atg cgc gat gat	1432
Ile Lys Ile Phe Cys Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp	
400 405 410	
gaa cgg aag cag ttt cga agg aag gtc aag tgc cca gac tcc agt aac	1480
Glu Arg Lys Gln Phe Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn	
415 420 425	
aat gca gga atc aag ggc tgc ctg ctg tca ggc ttc agg ggc aat gag	1528
Asn Ala Gly Ile Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu	
430 435 440	
acc aca tac ttg cgg cca gaa act gac ctg gag acc cag cct gtg ttg	1576
Thr Thr Tyr Leu Arg Pro Glu Thr Asp Leu Glu Thr Gln Pro Val Leu	
445 450 455	
ttt atc ccc aat ctg cat ttt tcc agc cta cag cgc cca gga ggg gtt	1624
Phe Ile Pro Asn Leu His Phe Ser Ser Leu Gln Arg Pro Gly Gly Val	
460 465 470 475	
gtc ccc tca gca gga cac agc agc tct gac agg ctg cct ctg aag cga	1672
Val Pro Ser Ala Gly His Ser Ser Asp Arg Leu Pro Leu Lys Arg	
480 485 490	
acc tgc tca ccc ttt gct gag gag ttt gag cct ctt cct tct aaa caa	1720
Thr Cys Ser Pro Phe Ala Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln	
495 500 505	
gcc aag gaa gat gac ctt cag aga gtt ctg ttg tat gtg agg agg gag	1768
Ala Lys Glu Asp Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu	
510 515 520	
aca gag gag gtg ttt gac gcg ctc atg ttg aag acc ccg gac ctg aag	1816
Thr Glu Glu Val Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys	
525 530 535	
ggc ctg agg aat gcg atc tct gag aag tac ggc ctc ccc gag gag aat	1864
Gly Leu Arg Asn Ala Ile Ser Glu Lys Tyr Gly Leu Pro Glu Glu Asn	
540 545 550 555	
att tgc aaa gtc tac aag aaa tgc aag cga ggc atc ctg gtt aac atg	1912
Ile Cys Lys Val Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met	
560 565 570	
gac aac aac atc atc caa cac tac agc aac cac gtg gcc ttc ctg ctg	1960
Asp Asn Asn Ile Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu	

DAVI251.001APC_sequence listing.TXT
 575 580 585

gac atg ggt gag ctg gac ggc aag atc cag atc atc ctg aag gag cta	2008
Asp Met Gly Glu Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu	
590 595 600	
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tctgtgtcag ctgttacttg aaatgcctt ctttggaaa gaggtctcgc aagcaaccaa	2128
ctcggtgatg tccaagccag ggagagacca agaaggttcc agatctaaa tgtcccaccc	2188
aggctcgaac tcactccaga gcttcctgaa agcacccagc ccaccggaga gtctgagcaa	2248
cacagaccca actgcctgct ttctttcta agtcccgtg cagaggccct tacagggac	2308
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tgccacctac tgggttacac atttcttatt tacagtttc attatgtat tatatatata	2608
tatatgtaaatattat gtacatatat gcaacatttt gtatgtccat gttacatttt	2668
tatcatttca aaaatatgtt tttcatattt cttgaactat ttttttagct gttattcgat	2728
tatgcattttt gtatatcata gggtttagta ataaaagcct acccatgcac acttaaaaaaa	2788
aaaaaaaaaa aaatatcnag cttatcgata ccgtcgaccc cga	2831

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<400> 16

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Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met Met
 35 40 45

Arg Val Asn Gly Asp Glu Glu Ser Val Ala Ala Leu Ser Phe Leu Tyr
 50 55 60

Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile Leu Ser Ser Ser Thr
 65 70 75 80

DAVI251.001APC_sequence listing.TXT
Gly Gly Arg Asn Asp Gln Gly Lys Lys Phe Tyr His Ser Met Asp Tyr
85 90 95

Glu Pro Asp Leu Ala Pro Leu Glu Ser Pro Thr His Leu Met Lys Phe
100 105 110

Leu Thr Glu Asn Val Ser Gly Ser Pro Asp Tyr Thr Asp Gln Leu Lys
115 120 125

Lys Asn Asn Leu Leu Gly Leu Glu Gly Val Leu Pro Thr Pro Gly Lys
130 135 140

Thr Asn Thr Val Pro Pro Gly Pro Ser Lys Leu Glu Ala Ser Ser Met
145 150 155 160

Asp Ser Tyr Leu Leu Pro Ala Ser Asp Ile Tyr Asp Asn Gly Ser Leu
165 170 175

Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro Pro Thr Gln Arg Trp
180 185 190

Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln Glu Ser Leu Leu Phe
195 200 205

Pro Asp Ile Leu Lys Thr Ser Pro Asp Pro Pro Cys Pro Glu Asp Tyr
210 215 220

Pro Gly Leu Lys Ser Asp Phe Glu Tyr Thr Leu Gly Ser Pro Lys Ala
225 230 235 240

Ile His Ile Lys Ala Gly Glu Ser Pro Met Ala Tyr Leu Asn Lys Gly
245 250 255

Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala Gly Gly Lys Gly Leu
260 265 270

Ala Leu Ser Ser Ser Lys Val Lys Ser Val Val Met Val Val Phe Asp
275 280 285

Asn Asp Lys Val Pro Val Glu Gln Leu Arg Phe Trp Arg His Trp His
290 295 300

Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile Asp Val Ala Asp Cys
305 310 315 320

Lys Glu Asn Phe Asn Thr Val Gln His Ile Glu Glu Val Ala Tyr Asn
325 330 335

DAVI251.001APC_sequence listing.TXT

Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu Ala Lys Val Phe Ile
340 345 350

Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val Lys
355 360 365

Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr Asp Cys Gly Ala Gly
370 375 380

Thr Glu Arg Leu Val His Arg Ala Val Cys Gln Ile Lys Ile Phe Cys
385 390 395 400

Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp Glu Arg Lys Gln Phe
405 410 415

Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn Asn Ala Gly Ile Lys
420 425 430

Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr Thr Tyr Leu Arg
435 440 445

Pro Glu Thr Asp Leu Glu Thr Gln Pro Val Leu Phe Ile Pro Asn Leu
450 455 460

His Phe Ser Ser Leu Gln Arg Pro Gly Gly Val Val Pro Ser Ala Gly
465 470 475 480

His Ser Ser Ser Asp Arg Leu Pro Leu Lys Arg Thr Cys Ser Pro Phe
485 490 495

Ala Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala Lys Glu Asp Asp
500 505 510

Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr Glu Glu Val Phe
515 520 525

Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly Leu Arg Asn Ala
530 535 540

Ile Ser Glu Lys Tyr Gly Leu Pro Glu Glu Asn Ile Cys Lys Val Tyr
545 550 555 560

Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp Asn Asn Ile Ile
565 570 575

Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp Met Gly Glu Leu
580 585 590

DAVI251.001APC_sequence listing.TXT

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 <212> DNA
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 gcagcaacat caaatgttag gccaaaatgc acaaaccgccc agcaacaaag gcagcaccaa 180
 gcgaacgaaa caacaacagc tccacatacc acaaagagtgc gcacattaga agcggccaaa 240
 agcagccagc cgagagcatt gtgttaagcca aaggcccaga gagccaggct aaaagcccc 300
 agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc 360
 accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca 420
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 atcctcacca agtgcacaaa tccgcattcct gatcccaaga gctcaaggca ccccgcccc 600
 aaattttagt gagaacgaaa cgaaggaagt tccttagtgc catagaaagc agttaatgaa 660
 acaacgacta agacgaagat cgaccatcca gaaccggagg gagctaattg cgaacgaaag 720
 aaaccacaaa gtgccttcca tcaatccgtt gataagtgtat atttattatg tttatacttg 780
 ccagcagccg aggcagcaac agcaatagca acaaccatag gggatcacgg catcgatgat 840
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DAVI251.001APC_sequence listing.TXT

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DAVI251.001APC_sequence listing.TXT

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DAVI251.001APC_sequence listing.TXT

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Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
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Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
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Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
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Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
100 105 110

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
115 120 125

Val Met Pro Ala Asp Gly Gly Gly Asn Asn Ser Asp Glu Gly His
130 135 140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
145 150 155 160

Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
165 170 175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
180 185 190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
195 200 205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser
210 215 220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met
225 230 235 240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
245 250 255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
260 265 270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
275 280 285

DAVI251.001APC_sequence listing.TXT

His Lys Lys His Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
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Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
325 330 335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile
340 345 350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
355 360 365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu
370 375 380

Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
385 390 395 400

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
405 410 415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
420 425 430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ala
435 440 445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
450 455 460

Gln
465 470 475 480

Gln His Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
485 490 495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
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Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
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Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly

DAVI251.001APC_sequence listing.TXT
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565 570 575

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580 585 590

Thr Thr Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg
595 600 605

Pro Trp His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile
610 615 620

Pro Lys Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro
625 630 635 640

Ile Ser Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn
645 650 655

Lys Gly Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu
660 665 670

Lys Pro Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe
675 680 685

Arg Glu Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp
690 695 700

His Ser Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr
705 710 715 720

Lys Asn Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn
725 730 735

Ala Ile Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn
740 745 750

Ile Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
755 760 765

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp Thr
770 775 780

DAVI251.001APC_sequence listing.TXT
Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys
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Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala Ala Lys Arg
805 810 815

Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu Leu Tyr His Pro
820 825 830

Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln Asp Phe Ala Lys Pro
835 840 845

Pro Val Leu Phe Ser Pro Ala Glu Asp Met Glu Lys Val Gly Gln Leu
850 855 860

Gly Ile Gly Ala Ala Thr Gly Met Thr Phe Asn Pro Leu Ser Asn Gly
865 870 875 880

Asn Ser Asn Ser Asn Ser His Ser Ser Leu Gln Ser Phe Tyr Gly His
885 890 895

Glu Thr Asp Ser Pro Asp Leu Lys Gly Ala Ser Pro Phe Leu Leu His
900 905 910

Gly Gln Lys Val Ala Thr Pro Thr Leu Lys Phe His Asn His Phe Pro
915 920 925

Pro Asp Met Gln Thr Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met
930 935 940

Leu Thr Ser Thr Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg Gly
945 950 955 960

Arg Met Thr Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg Gln
965 970 975

Glu Asn Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr Thr
980 985 990

Ile Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr Thr
995 1000 1005

Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala
1010 1015 1020

Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile
1025 1030 1035

DAVI251.001APC_sequence listing.TXT

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Thr Leu Thr Glu Leu Pro Asn Gln
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DAVI251.001APC_sequence listing.TXT

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DAVI251.001APC_sequence listing.TXT

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DAVI251.001APC_sequence listing.TXT

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DAV1251.001APC_sequence listing.TXT

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gtctcgat当地 cgctccctg cttatgat当地 gaccttaggt ccagggcaag tatgagttac	4500
cgaatctatc tattaggtgc atctaacgaa aggaatcatt agctctgc当地 gaactctagc	4560
cgtat当地 tgc当地 atctat当地 ttgtat当地 ggcttaagcg tttactt当地 tgc当地	4620
gtgtaaaattt当地 atttt当地 gaaaacc cacacaaaac acaaatcgat当地 tgc当地	4680
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<211> 1030

<212> PRT

<213> Drosophila

<400> 35

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Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His
20 25 30

Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
35 40 45

Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
50 55 60

Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
65 70 75 80

Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
85 90 95

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
100 105 110

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
115 120 125

Val Met Pro Ala Asp Gly Gly Gly Asn Asn Ser Asp Glu Gly His
130 135 140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
145 150 155 160

Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
165 170 175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
180 185 190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
195 200 205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser

DAVI251.001APC_sequence_listing.TXT
210 215 220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met
225 230 235 240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
245 250 255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
260 265 270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
275 280 285

His Lys Lys His Ala Ala Ala Ala Ala Ala Gly Gly Ser
290 295 300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu
305 310 315 320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
325 330 335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile
340 345 350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
355 360 365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu
370 375 380

Pro Tyr Ala Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
385 390 395 400

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
405 410 415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
420 425 430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala
435 440 445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Ile Ser His His
450 455 460

DAVI251.001APC_sequence_listing.TXT

Gln His Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
485 490 495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
500 505 510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
515 520 525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly
530 535 540

Pro Gly Ser Val Ile Thr Gln Lys Ser Phe Asp Tyr Thr Glu Leu Cys
545 550 555 560

Gln Pro Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val
565 570 575

Asn Ser Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro
580 585 590

Thr Thr Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg
595 . 600 . 605

Pro Trp His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile
610 615 620

Pro Lys Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro
625 630 635 640

Ile Ser Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn
645 650 655

Lys Gly Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu
660 665 670

Lys Pro Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe
675 680 685

Arg Glu Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp
690 695 . 700

His Ser Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr
705 710 715 720

DAVI251.001APC_sequence listing.TXT

Lys Asn Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn
725 730 735

Ala Ile Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn
740 745 750

Ile Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
755 760 765

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp Thr
770 775 780

Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys
785 790 795 800

Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala Ala Lys Arg
805 810 815

Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu Leu Tyr His Pro
820 825 830

Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln Asp Phe Ala Lys Pro
835 840 845

Pro Val Leu Phe Ser Pro Ala Glu Asp Met Glu Lys Ser Phe Tyr Gly
850 855 860

His Glu Thr Asp Ser Pro Asp Leu Lys Gly Ala Ser Pro Phe Leu Leu
865 870 875 880

His Gly Gln Lys Val Ala Thr Pro Thr Leu Lys Phe His Asn His Phe
885 890 895

Pro Pro Asp Met Gln Thr Asp Lys Lys Asp His Ile Leu Asp Gln Asn
900 905 910

Met Leu Thr Ser Thr Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg
915 920 925

Gly Arg Met Thr Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg
930 935 940

Gln Glu Asn Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr
945 950 955 960

Thr Ile Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr
965 970 975

DAVI251.001APC_sequence listing.TXT

Thr Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala
 980 985 990

Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile Phe
 995 1000 1005

Leu Leu Glu Val Gln Gln Ile Glu Asp Asp Leu Tyr Asp Val Thr
 1010 1015 1020

Leu Thr Glu Leu Pro Asn Gln
 1025 1030

<210> 36
 <211> 5650
 <212> DNA
 <213> Drosophila

<400> 36		
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gcagcaacat caaatgttag gccaaaatgc acaaaccgccc agcaacaaag gcagcaccaa	180	
gcgaacgaaa caacaacagc tccacatacc acaaagagtg gcacattaga agcggccaaa	240	
agcagccagc cgagagcatt gtgttaagcca aaggcccaga gagccaggct aaaagcccc	300	
agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc	360	
accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca	420	
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cagtccacga ccaagtccctt gtgcaatccg gaatccagtt caaatttagtt caataagccg	900	
tatctaccac gtataatgtc cacatccacc gccacaacga gcgttatcac gtccaacgag	960	
ctctcgctgt ccggccacgc ccacggcac ggtcacgccc accagttgca ccagcacacc	1020	
cacagccgcc taggagttgg cgtttgttt ggcatccctt ggcacgcac cctatgccc	1080	
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DAVI251.001APC_sequence listing.TXT

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ggtggcaata	attccgatga	aggtcatgcc	atcgatgcgc	ggattgcggc	ccaaatgggc	1380
aaccaagccc	agcaaacagca	gcagcagcaa	cagcagacgg	aacaccagcc	gctggccaag	1440
atcgagttcg	atgagaacca	gataatccgg	gtggtgggac	caaatggcga	gcaacagcaa	1500
atcatctcgc	gggagatcat	caatggggag	catcatatcc	tgtcgcaaaa	cgaggctggt	1560
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gtggccacgg	ccatgtacaa	ccaggccaa	aagatgaaca	atgatcacgg	gcaggcggta	1680
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aatgtgaaac	aactgccccca	tttgacggta	ccccaaaaac	ttgatcccga	cctctatcaa	1920
gccgataagc	atatagattt	gatctacaac	gatggcagca	agacggtgat	ttactccact	1980
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DAV1251.001APC_sequence listing.TXT

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gacgatgaca	tgatatcgtt	ctactgcaac	gaggacatct	ttctgctgga	ggtgcaacag	4860
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DAVI251.001APC_sequence listing.TXT

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ataataatgg gatccgcaac aaatcgagtt gcaacgaatg ttaagaacgc taacacaata	5100
cgcatgtaaa atgatacttt aaaattgatt tagttatccc agcaacaatg agattatcta	5160
aaattgtttg atcaaatttt acattctcgc tatgtctata gataattcta agcccgtaa	5220
cccataagcg taatcgtaat cgtaatcgta ccgtgtatcc atgctcatat ataaacaact	5280
atatatatat atatatatat atatatgtgc ggagtgcac agtgtctgtc cagtaggaga	5340
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agccgtagcc tattgtatc cattgtatg tttggctaa gcgtttact tggtgaatat	5520
aaagtgtaaa attattttg aaaaaaaaaa acccacacaa aacacaaatc gttgttcta	5580
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<210> 37

<211> 1331

<212> PRT

<213> Drosophila

<400> 37

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Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His
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Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
 35 40 45

Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
 50 55 60

Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
 65 70 75 80

Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
 85 90 95

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
 100 105 110

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
 115 120 125

DAVI251.001APC_sequence listing.TXT

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His
130 135 140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
145 150 155 160

Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
165 170 175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
180 185 190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
195 200 205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser
210 215 220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met
225 230 235 240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
245 250 255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
260 265 270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
275 280 285

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
290 295 300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu
305 310 315 320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
325 330 335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile
340 345 350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
355 360 365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu

DAVI251.001APC_sequence listing.TXT
375 380

Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
385 390 395 400

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
405 410 415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
420 425 430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala
435 440 445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
450 455 460

Gln
465 470 475 480

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
485 490 495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
500 505 510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
515 520 525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly
530 535 540

Pro Gly Ser Val Ile Thr Gln Lys Ile Leu His Val Asp Ala Pro Thr
545 550 555 560

Ala Ser Glu Ala Asp Arg Pro Ser Thr Pro Ser Ser Ser Ile Asn Ser
565 570 575

Thr Glu Asn Thr Glu Ser Asp Ser Gln Ser Val Ser Gly Ser Glu Ser
580 585 590

Gly Ser Pro Gly Ala Arg Thr Thr Ala Thr Leu Glu Met Tyr Ala Thr
595 600 605

Thr Gly Gly Thr Gln Ile Tyr Leu Gln Thr Ser His Pro Ser Thr Ala
610 615 620

DAVI251.001APC_sequence listing.TXT
Ser Gly Ala Gly Gly Gly Ala Gly Pro Ala Gly Ala Ala Gly Gly Gly
625 630 635 640
Gly Val Ser Met Gln Ala Gln Ser Pro Ser Pro Gly Pro Tyr Ile Thr
645 650 655
Ala Asn Asp Tyr Gly Met Tyr Thr Ala Ser Arg Leu Pro Pro Gly Pro
660 665 670
Pro Pro Thr Ser Thr Thr Phe Ile Ala Glu Pro Ser Tyr Tyr Arg
675 680 685
Glu Tyr Phe Ala Pro Asp Gly Gln Gly Gly Tyr Val Pro Ala Ser Thr
690 695 700
Arg Ser Leu Tyr Gly Asp Val Asp Val Ser Val Ser Gln Pro Gly Gly
705 710 715 720
Val Val Thr Tyr Glu Gly Arg Phe Ala Gly Ser Val Pro Pro Pro Ala
725 730 735
Thr Thr Thr Val Leu Thr Ser Val His His His Gln Gln Gln Gln Gln
740 745 750
Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln His His Gln
755 760 765
Gln Gln Gln His His Ser Gln Asp Gly Lys Ser Asn Gly Gly Ala Thr
770 775 780
Pro Leu Tyr Ala Lys Ala Ile Thr Ala Ala Gly Leu Thr Val Asp Leu
785 790 795 800
Pro Ser Pro Asp Ser Gly Ile Gly Thr Asp Ala Ile Thr Pro Arg Asp
805 810 815
Gln Thr Asn Ile Gln Gln Ser Phe Asp Tyr Thr Glu Leu Cys Gln Pro
820 825 830
Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val Asn Ser
835 840 845
Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro Thr Thr
850 855 860
Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg Pro Trp
865 870 875 880

DAVI251.001APC_sequence listing.TXT

His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile Pro Lys
885 890 895

Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro Ile Ser
900 905 910

Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn Lys Gly
915 920 925

Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu Lys Pro
930 935 940

Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe Arg Glu
945 950 955 960

Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp His Ser
965 970 975

Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr Lys Asn
980 985 990

Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn Ala Ile
995 1000 1005

Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn Ile
1010 1015 1020

Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
1025 1030 1035

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp
1040 1045 1050

Thr Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys
1055 1060 1065

Asp Lys Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala
1070 1075 1080

Ala Lys Arg Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu
1085 1090 1095

Leu Tyr His Pro Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln
1100 1105 1110

Asp Phe Ala Lys Pro Pro Val Leu Phe Ser Pro Ala Glu Asp Met
1115 1120 1125

DAVI251.001APC_sequence listing.TXT

Glu Lys Val Gly Gln Leu Gly Ile Gly Ala Ala Thr Gly Met Thr
1130 1135 1140

Phe Asn Pro Leu Ser Asn Gly Asn Ser Asn Ser Asn Ser His Ser
1145 1150 1155

Ser Leu Gln Ser Phe Tyr Gly His Glu Thr Asp Ser Pro Asp Leu
1160 1165 1170

Lys Gly Ala Ser Pro Phe Leu Leu His Gly Gln Lys Val Ala Thr
1175 1180 1185

Pro Thr Leu Lys Phe His Asn His Phe Pro Pro Asp Met Gln Thr
1190 1195 1200

Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met Leu Thr Ser Thr
1205 1210 1215

Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg Gly Arg Met Thr
1220 1225 1230

Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg Gln Glu Asn
1235 1240 1245

Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr Thr Ile
1250 1255 1260

Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr Thr
1265 1270 1275

Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala
1280 1285 1290

Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile
1295 1300 1305

Phe Leu Leu Glu Val Gln Gln Ile Glu Asp Asp Leu Tyr Asp Val
1310 1315 1320

Thr Leu Thr Glu Leu Pro Asn Gln
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<210> 38
<211> 5557
<212> DNA
<213> Drosophila

DAVI251.001APC_sequence listing.TXT

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DAVI251.001APC_sequence_listing.TXT

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DAVI251.001APC_sequence listing.TXT

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DAVI251.001APC_sequence listing.TXT

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<212> PRT

<213> Drosophila

<400> 39

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Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
35 40 45

Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
50 55 60

Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
65 70 75 80

Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
85 90 95

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
100 105 110

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
115 120 125

Val Met Pro Ala Asp Gly Gly Gly Asn Asn Ser Asp Glu Gly His
130 135 140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
145 150 155 160

Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
165 170 175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
180 185 190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
195 200 205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser
210 215 220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met

225

DAVI251.001APC_sequence listing.TXT

230

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240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
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Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
260 265 270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
275 280 285

His Lys Lys His Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
290 295 300

Ile Ile Tyr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu
305 310 315 320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
325 330 335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile
340 345 350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
355 360 365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu
370 375 380

Pro Tyr Ala Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
385 390 395 400

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
405 410 415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
420 425 430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ala
435 440 445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
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Gln
465 470 475 480

DAVI251.001APC_sequence listing.TXT
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485 490 495
Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
500 505 510
Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
515 520 525
Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly
530 535 540
Pro Gly Ser Val Ile Thr Gln Lys Ile Leu His Val Asp Ala Pro Thr
545 550 555 560
Ala Ser Glu Ala Asp Arg Pro Ser Thr Pro Ser Ser Ser Ile Asn Ser
565 570 575
Thr Glu Asn Thr Glu Ser Asp Ser Gln Ser Val Ser Gly Ser Glu Ser
580 585 590
Gly Ser Pro Gly Ala Arg Thr Thr Ala Thr Leu Glu Met Tyr Ala Thr
595 600 605
Thr Gly Gly Thr Gln Ile Tyr Leu Gln Thr Ser His Pro Ser Thr Ala
610 615 620
Ser Gly Ala Gly Gly Ala Gly Pro Ala Gly Ala Ala Gly Gly
625 630 635 640
Gly Val Ser Met Gln Ala Gln Ser Pro Ser Pro Gly Pro Tyr Ile Thr
645 650 655
Ala Asn Asp Tyr Gly Met Tyr Thr Ala Ser Arg Leu Pro Pro Gly Pro
660 665 670
Pro Pro Thr Ser Thr Thr Phe Ile Ala Glu Pro Ser Tyr Tyr Arg
675 680 685
Glu Tyr Phe Ala Pro Asp Gly Gln Gly Gly Tyr Val Pro Ala Ser Thr
690 695 700
Arg Ser Leu Tyr Gly Asp Val Asp Val Ser Val Ser Gln Pro Gly Gly
705 710 715 720
Val Val Thr Tyr Glu Gly Arg Phe Ala Gly Ser Val Pro Pro Pro Ala
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DAVI251.001APC_sequence listing.TXT

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Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln His His Gln
755 760 765

Gln Gln Gln His His Ser Gln Asp Gly Lys Ser Asn Gly Gly Ala Thr
770 775 780

Pro Leu Tyr Ala Lys Ala Ile Thr Ala Ala Gly Leu Thr Val Asp Leu
785 790 795 800

Pro Ser Pro Asp Ser Gly Ile Gly Thr Asp Ala Ile Thr Pro Arg Asp
805 810 815

Gln Thr Asn Ile Gln Gln Ser Phe Asp Tyr Thr Glu Leu Cys Gln Pro
820 825 830

Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val Asn Ser
835 840 845

Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro Thr Thr
850 855 860

Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg Pro Trp
865 870 875 880

His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile Pro Lys
885 890 895

Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro Ile Ser
900 905 910

Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn Lys Gly
915 920 925

Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu Lys Pro
930 935 940

Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe Arg Glu
945 950 955 960

Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp His Ser
965 970 975

Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr Lys Asn
980 985 990

DAVI251.001APC_sequence listing.TXT

Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn Ala Ile
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Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn Ile
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Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
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Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp
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Thr Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys
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Asp Lys Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala
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Ala Lys Arg Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu
1085 1090 1095

Leu Tyr His Pro Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln
1100 1105 1110

Asp Phe Ala Lys Pro Pro Val Leu Phe Ser Pro Ala Glu Asp Met
1115 1120 1125

Glu Lys Val Gly Gln Leu Gly Ile Gly Ala Ala Thr Gly Met Thr
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Phe Asn Pro Leu Ser Asn Gly Asn Ser Asn Ser Asn Ser His Ser
1145 1150 1155

Ser Leu Gln Ser Phe Tyr Gly His Glu Thr Asp Ser Pro Asp Leu
1160 1165 1170

Lys Gly Ala Ser Pro Phe Leu Leu His Gly Gln Lys Val Ala Thr
1175 1180 1185

Pro Thr Leu Lys Phe His Asn His Phe Pro Pro Asp Met Gln Thr
1190 1195 1200

Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met Leu Thr Ser Thr
1205 1210 1215

Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg Gly Arg Met Thr

1220

DAVI251.001APC_sequence Listing.TXT
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Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr Thr
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Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala
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Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile
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DAVI251.001APC_sequence listing.TXT

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